

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: April 23, 2003, 13:00:00 ; Search time 22 Seconds
(without alignments)
2543.192 Million cell updates/sec

Title: US-09-635-949-34

Perfect score: 3289

Sequence: 1 MDELALIVLSSLYLQAAAF.....TGLGLDDVSIKKKCHSEER 582

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1066.5	32.4	558	2 T17324	hypothetical prote
2	406.5	12.4	2871	2 A55567	fibrillin 1 - bovi
3	402	12.2	1221	2 A49457	fibrillin-2 precurs
4	398.5	12.1	2871	2 A55624	fibrillin-1 precur
5	397.5	12.1	2918	2 A54105	fibrillin-2 precur
6	397	12.1	2907	2 A57278	fibrillin-1 precur
7	395.5	12.0	3002	2 A47221	fibrillin-2 precurs
8	381.5	11.6	1184	2 A55184	fibrillin-1 precur
9	375.5	11.4	1574	2 T13954	MEGF6 protein - ra
10	357	10.9	1620	2 T27283	hypothetical prote
11	346	10.5	3507	2 T34513	hypothetical prote
12	340	10.3	683	2 C36346	fibrulin 1 precursor
13	338	10.3	601	2 B36346	fibrulin 1 precursor
14	334.5	10.2	685	2 S78040	fibrulin, splice fo
15	332	10.1	705	2 S34968	fibrulin, splice fo
16	327	9.9	589	2 T43210	fibrulin-ID precurs
17	327	9.9	689	2 T42760	fibrulin, splice fo
18	327	9.9	741	2 T46488	hypothetical prote
19	325	9.9	712	2 T42990	fibrulin 1, splice
20	324.5	9.9	798	2 T22793	hypothetical prote
21	315.5	9.6	2555	2 A40043	notch protein homo
22	310.5	9.4	2524	2 A35844	notch protein - Af
23	308	9.4	2531	2 A46019	Notch-1 protein -
24	307	9.3	1247	1 MMHUND	nidogen precursor
25	304	9.2	1820	2 A55494	latent transformin
26	301	9.2	493	2 JC5621	epidermal growth f
27	297	9.0	2531	2 S18188	notch protein homo
28	296	9.0	1712	2 A38261	masking protein pr
29	295.5	9.0	1394	2 A35626	transforming growth

30 295 9.0 387 2 138449 extracellular prot
31 293.5 8.9 2321 2 S78549 notch3 protein - h
32 290.5 8.8 1964 2 T09059 notch4 - mouse
33 288 8.8 1106 2 T18739 hypothetical prote
34 287 8.7 1245 1 MMSND nidogen precursor
35 286 8.7 2437 2 S42612 transmembrane prot
36 285.5 8.7 810 2 T10756 Not-homolog protei
37 285.5 8.7 1376 2 G00043 osteonidogen - hum
38 283 8.6 1251 2 A57293 latent transformin
39 281 8.5 2318 2 S45306 notch 3 protein -
40 280.5 8.5 728 2 T50719 c-Delta-1 - chicke
41 279.5 8.5 2703 1 A24420 notch protein - fr
42 278 8.5 1220 2 A56136 jagged protein pre
43 275 8.4 577 2 A60501 thrombomodulin pre
44 273.5 8.3 886 2 A57172 probable hormone r
45 272.5 8.3 356 2 A25918 thrombomodulin - b

ALIGNMENTS

RESULT 1

T17324

hypothetical protein DKFZp564P2063.1 - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T17324

R:Dueterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, September 1999

A:Reference number: Z18727

A:Accession: T17324

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-558 <DUE>

A:Cross-references: EMBL:AL117610

A:Experimental source: fetal brain; clone DKFZp564P2063

C:Genetics:

A:Note: DKFZp564P2063.1

Query Match 32.4% Score 1066.5; DB 2: Length 558;
Best Local Similarity 37.5% Pred. No. 1.2e-51;
Matches 214; Conservative 95; Mismatches 175; Indels 87; Gaps 15;

Qy 34 GICRYGGRIDCCGWARSGCQCQPPYVIRORIARICQI:KAVCQPRCKHGECIGPNKCK 93

Db 44 GVCHYGTKLACCYGWRNRNSKGVE-----ATCEPGCKFGECVGNPKCR 86

Qy 94 CHPGYAGTCTLOVLFECGLKPRCKHRCMNITYGSYKVCYCLNGYIMPDGSCSSALTCSMA 153

Db 87 CLPGYTGKTCSDQVNECGMKPRPCOHCRCVNTGHSYKCKCLSGHMLMPDTCVYSKTCAM 146

Qy 154 NCQYGCDDVVGQIRQCQCPSPGLQAPDGRCTVDVDECATGRASCPRPQCQVNTFGSYICK 213

Db 147 NCQYSCDETEGPOCLCFSSGIRLAPNGRCDIDECASGVICYNKRCVNTFGSYICK 206

Qy 214 CHKGFDMYIGKKYQCHDIDECISGQYQCSSFANCYVNRGYSYKCKKCYGCGDGLTCVYI 273

Db 207 CHIGFELYISGRVDCIDINECTMDSHTSSHHANCFNTGGSFCKCKQGYKGNGLRCSAI 266

Qy 274 PKVMIERPSPHVPKNGNTILKGDGTNNMWIPDVGSTWPPKTPYIPPLINRPTSKPTT 333

Db 267 PENSVK-----EVLRAPGTI-----KDKIKKLAHKNSMKKA 299

Qy 334 R---PTPKPTPIPPPPPPPLTELRTPLPPTTPERTPTTGLTTIAPAASSTPPG----- 383

Db 300 KIKVNTPTPTPTP-----KVMIQPNFV-----GI---VSRGSGSGGKKGKNEK 343

Qy 384 ---GITVDNRVQ-----TDFQKPRGDVFIIPQPSNDI:FEIPEIERCVSADAEAKDDPCV 434

Db 344 MKEGLEDEKREKALKNDIEERSLRGDDVFFPKVNEAGEFGLIVRKALTSKLEHKDLNI 403

Qy 435 LVHSCNFDFHGLCCWIREKNDLHWEPTI-RDPAGCOYLITVSAAKAPGGKAANI:VILPIGRIM 493

Db 404 SV-DCSFNHCIDMKQKOURDEHDFMNPADPRDINAIGFYMAVPALAGHKKIDIGRIKLLIPDILQ 462
 QY 494 HSGDLCLSFRIHKVTGLHSITLOWFVRKUGAAGALGRNGGHHG--WRQTOITL-RGAD-I 549
 Db 463 PQSNFCSLDYRLAGDKVKLRVFK--NSNNALAEKTISEDEKWKTKGIQLYQGTDAT 520
 QY 550 KSVVPKGEKRRKRGHTGIEGLIDVSLKKGHCHSE 580
 Db 521 KSIIFVAERKGGKTGETLAVDGVLLVSLGLCPD 551

RESULT 2
 A: fibulin-1 - bovine
 C: Species: Bos primigenius taurus (cattle)
 C: Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 02-Aug-2002
 C: Accession: A55567
 R: Tilsstra, D.J.; Li, L.; Potter, K.A.; Womack, J.; Myers, P.H.
 Genomics 23, 480-485, 1994
 A: Title: Sequence of the coding region of the bovine fibulin cDNA and localization to
 A: Reference number: A55567; MUID:95137597; PMID:7835900
 A: Accession: A55567
 A: Status: preliminary
 A: Molecule type: mRNA
 A: Residues: 1-2871 <TILL>
 A: Cross-references: GR:L28748; NID:q508427; PIDN:AAA74122.1; PID:q508428
 C: Superfamily: fibulin-1; EGF homology
 F:1201-1236/Domain: EGF homology <EGF>

Query Match 12.4%; Score 406.5; DB 2: Length 2871;
 Best local Similarity 32.0%; Pred. No. 8.5e-15;
 Matches 105; Conservative 32; Mismatches 104; Indels 87; Gaps 15;

QY 35 LCRVY-----GRIDCGWQWARGSWGQCPFYVLRRIARI-----RCOLKAVCPCKKGG 84
 Db 1123 LCRGVCLNTEGYSR-----KCPYGHQIAINISACIDINNECELSA-----HFCPRG 1169
 QY 85 EC---IGPNKKCKHPGYAGKT-----CIQVLNEGLKPRCKHRCMNTYGSYKCYCLNGYM 137
 Db 1170 RCVNLIIGKYQACNPGYHSTPDLFCVDI-DECSINMGCECTETNSGSEYSCSGCPGFA 1228
 QY 138 LMPD-GSCSSALTC--SMANCOYG-CDVVKGQIRKCCPSGIGLADPGRCTVIV-----187
 Db 1229 LMPDQRSCDIDDECDNPNICDGGQCTNIPGYRCLC-YDGFMASEDMTKTVDNPCDLIN 1287
 QY 188 -----DECATGRASCPREFRCQCVNTFGSYI 211
 Db 1288 PNICLSCTGENTKSPICHCMDMGYSKKKGTCTGCTDINECEIGAHNCDRAVCINTAGSPK 1347
 QY 212 CKCHKGFDLAMYIGKYGCHDIDPCSLGOVCSFANCVNVRGSKCKKPKGQCGDGLTCV 271
 Db 1348 CSCSPG-----WIGDGKCTDLDECSNCTIMCSQHADCKNTMGSRCLCKEYGTGDTCT 1403
 QY 272 YIPKVMIEPSCPIHVPGKNTILKGDYG 299
 Db 1404 DLD-----ECSENLNL-CGNGCQCLNAPCG 1426

RESULT 3
 A: fibulin-2 precursor - mouse
 C: Species: Mus musculus (house mouse)
 C: Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 02-Aug-2002
 C: Accession: A49457; S74095
 R: Pan, T.C.; Sasaki, T.; Zhang, R.Z.; Faessler, R.; Timpl, R.; Chu, M.L.
 J. Cell Biol. 123, 1269-1277, 1993
 A: Title: Structure and expression of fibulin-2, a novel extracellular matrix protein with
 A: Reference number: A49457; MUID:94064787; PMID:8245130
 A: Accession: A49457
 A: Status: preliminary
 A: Molecule type: mRNA
 A: Residues: 1-1221 <PAN>
 A: Cross-references: GR:X75285; NID:q437046; PIDN:CAA53040.1; PID:q437047

R: Sasaki, T.; Mann, K.; Murphy, G.; Chu, M.L.; Timpl, R.
 Eur. J. Biochem. 240, 427-434, 1996
 A: Title: Different susceptibilities of fibulin-1 and fibulin-2 to cleavage by matrix
 A: Reference number: S74094; MUID:96439073; PMID:8841408
 A: Accession: S74095
 A: Molecule type: protein
 A: Residues: 236-238, X', 240-247; 260-275; 336-344, Y', 446-461; 405-426; 566-568, YPM', 569
 C: Superfamily: fibulin-2; EGF homology
 C: Keywords: calcium binding; duplication; extracellular matrix; glycoprotein; homotrimer
 F:942-978/Domain: EGF homology <EGF>

Query Match 12.2%; Score 402; DB 2: Length 1221;
 Best local Similarity 36.6%; Pred. No. 7.1e-15;
 Matches 93; Conservative 29; Mismatches 92; Indels 40; Gaps 14;

QY 80 RCKHGE-CI---GPNKKCKHPGYA-----GKTGIVLNEGLKPRCKHRCMNTYGSYK 130
 Db 905 RCGHGLCYNLPGSYKCKCKPQFQFADAFRTIDV-NFQWSPGRIQHTTENTTTSYRC 963
 QY 131 YCLNGYMLMPDGS-CSSALTCSMANCOYGCDVVKGQIRKCCPSGIGLADPGRCTVIV 189
 Db 964 SCANGFLAADCKHCEVDNECETBRCSECCANTYGSYCYC-RCGYLAEDGHTCTDDE 1022
 QY 190 CATGRASCPHRCQCVNTFGSYICKC-HKGFDMYIGKYGCTHDIHDSIGYQVCTSSPAC 248
 Db 1023 CAQAGCIICTER-CVNVPGSYQACPEQGYTMANG-RSCKDIDECALGTHNCEATTC 1079
 QY 249 YNVRSYK---CKEGY-----QGDGLTCVYIPKVMIEPSC-----PIH 285
 Db 1080 HNIQGSFRCIRPDPPNVVSVQTKCERTCODITFCQTSAPARTHYQINPOTGLLVPAH 1149
 QY 286 VPK-GNCTILKGP 298
 Db 1140 IFRIGPAPAFAGDT 1153

RESULT 4
 A: fibulin-1 precursor - mouse
 C: Species: Mus musculus (house mouse)
 C: Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 02-Aug-2002
 C: Accession: A55624
 R: Yin, W.; Smiley, E.; Germiller, J.; Sanguinetti, C.; Lawton, T.; Pereira, L.; Ramire
 J. Biol. Chem. 270, 1798-1806, 1995
 A: Title: Primary structure and developmental expression of Fbn-1, the mouse fibulin
 A: Reference number: A55624; MUID:95130561; PMID:7829516
 A: Accession: A55624
 A: Status: preliminary
 A: Molecule type: mRNA
 A: Residues: 1-2871 <YIN>
 A: Cross-references: GB:L29454; NID:q575509; PIDN:AAA56840.1; PID:q575510
 C: Genetics:
 A: Gene: Fbn-1
 C: Superfamily: fibulin-1; EGF homology
 F:1201-1236/Domain: EGF homology <EGF>

Query Match 12.1%; Score 398.5; DB 2: Length 2871;
 Best local Similarity 31.7%; Pred. No. 2.4e-14;
 Matches 104; Conservative 33; Mismatches 104; Indels 87; Gaps 15;

QY 35 LCRVY-----GRIDCGWQWARGSWGQCPFYVLRRIARI-----RCOLKAVCPCKKGG 84
 Db 1123 LCRGGTCHNTEGYSR-----ECPPGHQISPNISACIDINNECELSA-----NLCPRG 1169
 QY 85 EC---IGPNKKCKHPGYAGKT-----TCIQLVNEGLKPRCKHRCMNTYGSYKCYCLNGYM 137
 Db 1170 RCVNLIIGKYQACNPGYHSTPDLFCVDI-DECSINMGCECTETNSGSEYSCSGCPGFA 1228
 QY 138 LMPD-GSCSSALTC--SMANCOYG-CDVVKGQIRKCCPSGIGLADPGRCTVIV-----187
 Db 1229 LMPDQRSCDIDDECDNPNICDGGQCTNIPGYRCLC-YDGFMASEDMTKTVDNPCDLIN 1287
 QY 188 -----DECATGRASCPREFRCQCVNTFGSYI 211
 Db 1288 PNICLSCTGENTKSPICHCMDMGYSKKKGTCTGCTDINECEIGAHNCDRAVCINTAGSPK 1347
 QY 212 CKCHKGFDLAMYIGKYGCHDIDPCSLGOVCSFANCVNVRGSKCKKPKGQCGDGLTCV 271
 Db 1348 CSCSPG-----WIGDGKCTDLDECSNCTIMCSQHADCKNTMGSRCLCKEYGTGDTCT 1403
 QY 272 YIPKVMIEPSCPIHVPGKNTILKGDYG 299
 Db 1404 DLD-----ECSENLNL-CGNGCQCLNAPCG 1426

Science 259, 680-683, 1993
 A:Title: The skipping of constitutive exons in vivo induced by nonsense mutations.
 A:Reference number: 159574; MUID:93157831; PMID:8430317
 A:Accession: 159574
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 2217-2288, 1', 2290-2325 <RES>
 A:Cross-references: GB:54426; NID:q264860; PIDN:AAB2544.1; PID:q264861
 A:Keywords: alternative splicing; calcium binding; extracellular matrix; glycoprotein; M
 A:Title: Connective tissue microfibrils. Isolation and characterization of three large p
 Nature 352, 330-334, 1991
 A:Title: Linkage of Marfan syndrome and a phenotypically related disorder to two differ
 A:Reference number: S17062; MUID:91304567; PMID:1852206
 A:Accession: S17062
 A:Molecule type: mRNA
 A:Residues: 'VIVVVFIFSYNKM', 944-1444 <LEF1>
 A:Cross-references: EMBL:X62008; NID:q31398; PIDN:CAH56534.1; PID:q5924015
 A:Accession: S62111
 A:Molecule type: protein
 A:Residues: 1166-1176, 'X', 1178-1180, 'D', 1182-1185 <LEE2>
 A:Keywords: alternative splicing; calcium binding; extracellular matrix; glycoprotein; M
 A:Title: Connective tissue microfibrils. Isolation and characterization of three large p
 A:Reference number: A34198; MUID:90078246; PMID:2512293
 A:Accession: A34198
 A:Molecule type: protein
 A:Residues: 565-575; 1890-1892, 'I', 1894-1900 <MAD>
 A:Comment: Fibrillin is a major component of elastin-associated microfibrils.
 C:Genetics:
 A:Gene: GDB:FBN1
 A:Cross-references: GDB:127115; OMIM:134797; OMIM:154700
 A:Map position: 15q21.1-15q21.1
 A:Introns: 2236/1; 2258/1; 2297/1
 C:Superfamily: fibrillin 1; EGF homology
 C:Keywords: alternative splicing; calcium binding; extracellular matrix; glycoprotein; M
 F:1-3002/Product: fibrillin (5'-region exon A splice form) (fragment) #status predicted
 F:1332-1367/Product: fibrillin (5'-region exon C splice form) (fragment) #status predicted
 F:1457-1492/Domain: EGF homology <EGF2>
 F:2262-2295/Domain: EGF homology <EGF1>
 Query Match 12.08; Score 395.5; DB 2; Length 3002;
 Best Local Similarity 31.4%; Pred. No. 3.5e-14;
 Matches 103; Conservative 34; Mismatches 104; Indels 87; Gaps 15;
 Qy 35 ICRYG-----GRIDCCGWARQWQCPYVLRQRIARI-----RCQIKAVCOPCKKHG B4
 Db 1254 ICRGVCHNTRGSYRC-----ECPPCHOI.SPNISACIDINEGLISA---HLCFNG 1300
 Qy 85 EC---IGPNKCKHPYAGKT-----CQVLNECGLKPPCKIIRKNTYGSYKCYCLNGYM 137
 Db 1301 KCVNIICKYOCACNPGYHSTHPIRIFCVDI-DECSIMNGGCTFTCTNSGSEYECSCQPCFA 1359
 Qy 138 LMPD-GSCSSALTC-SMANCOYG-QVWVKQI-RCQGFSPICLIQAPDGRICVDV-----187
 Db 1360 LMPDSCSDTDEEDNPNICDGGQCTNIPGEYRCLC-YGPFMASEDHMKTCVDVNECDLN 1418
 Qy 188 -----DPCATGRASCPFRQCNTPGSYI 211
 Db 1419 PNICISGTCENTKGSFICHCDMGYSKKKGTGCTDINPCEIGAHNCCKKHAVCNTIACSPK 1478
 Qy 212 CKKHGFDLWYIGKYQCHIDIDECSLQYQSSSFARCYNVKSGYKCKEYQGDGLTCV 271
 Db 1479 CSCSPG-----WIGDGIKTDTIDFESNCTHMCQSHADCKNTMGSYRCLCKEYTGIGFTCT 1534
 Qy 272 YIPKVMIEPSPGTHVPKNGNGLIAGDTG 299
 Db 1535 DLD-----ECSENLDL-CGNGQCLANPGG 1557
 RESULT 8
 A55184
 Fibrillin-2 precursor - human
 N:Alternate names: protein DKFZp586A1519.1

C:Species: Homo sapiens (man)
 C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 02 Aug 2002
 C:Accession: A55184; #08744
 R:Zhang, R.Z.; Pan, T.C.; Zhang, Z.Y.; Mattei, M.G.; Timpl, R.; Chu, M.H.
 Genomics 22, 425-430, 1994
 A:Title: Fibrillin-2 (FBN2): human cDNA sequence, mRNA expression, and mapping of the
 A:Reference number: A55184; MUID:95104955; PMID:7806230
 A:Accession: A55184
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1184 <ZHA>
 A:Cross-references: GB:X82494; NID:q575232; PIDN:CAA57876.1; PID:q575233
 R:Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, March 1999
 A:Reference number: Z16471
 A:Accession: T08744
 A:Molecule type: mRNA
 A:Residues: 656-719, 'QDECLMGAIHVSRRQFCVNTLGSFYCVNITVLCAKCYLLNRIKRCVD', 720-853, 'T', 855
 A:Cross-references: EMBL:AL050095
 A:Experimental source: adult uterus; clone DKFZp586A1519
 C:Genetics:
 A:Gene: GDB:FBN2
 A:Cross-references: GDB:293037; OMIM:135821
 A:Map position: 3p25-3p24
 A:Note: DKFZp586A1519.1
 C:Superfamily: fibrillin-2; EGF homology
 C:Keywords: alternative splicing; extracellular matrix
 F:1-27/Domain: signal sequence #status predicted <SIG>
 F:28-1184/Product: fibrillin-2 protein #status predicted <MAT>
 F:905-941/Domain: EGF homology <EGF>
 Query Match 11.6%; Score 381.5; DB 2; Length 1184;
 Best Local Similarity 34.4%; Pred. No. 9.2e-14;
 Matches 84; Conservative 29; Mismatches 91; Indels 40; Gaps 11;
 Qy 56 QPFYVLRQRIARICOLKAVCOPCKKH-----GEGLGNPKK-----CH PG 97
 Db 821 CRPGFSCINTVGSYTCORNLICARGYHSDGAKVDVNEETGVHRRGEGQVHNDPG HH0
 Qy 98 -----YAKTKIQVINEGCLKP-RCKKRCOMNTYGSYKCYCLNGYMLMKHS 143
 Db 881 SYRCDCKAGFORAFRGGLDV-NECWASPGRLCQHTCENTLGSYKCSASGELLANDCK 939
 Qy 144 -CSSALTCSMANCOYGQVWVKQIIRQCPSPGLQAPDGRICVDVDFATGRASCPFRPG 202
 Db 940 RCEVNECEAQRCSQCANIYGSVQCYC-RQGYLAKKHGCTDIDECAGAGILCTER 997
 Qy 203 CVNTFGSYICKKHGFDLWYIGKYQCHIDIDECSLQYQSSSFARCYNVKSGYK- KC 259
 Db 998 CLNVPGSYQACPEQSYTMTANGR-SCRDVDEALGTHNGSEATCTINIGSFCRLRPEC 1056
 Qy 260 KEGY 263
 Db 1057 PPNY 1060
 RESULT 9
 T13954
 MEGF6 protein - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21 Jul 2000
 C:Accession: T13954
 R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Saki, N.; Ohata, O.
 Genomics 51, 27-34, 1998
 A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motif
 A:Reference number: Z14126; MUID:98360089; PMID:9694040
 A:Accession: T13954
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1574 <NAK>
 A:Cross-references: EMBL:AH011532; NID:q4449293; PIDN:AAI2462.1; PID:q4449294
 A:Experimental source: strain Sprague bawley; brain
 C:Genetics:

A:Gene: MEGF6

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Query Match          11.4%   Score 375.5; DB 2; Length 1574;
Best local Similarity 35.5%; Pred. No. 2.5e-13;
Matches 94; Conservative 28; Mismatches 98; Indels 45; Gaps 14;

QY  44  CCWCARQSGWQCQPFFVYLRRIARICQLKAVQCPCKKHGECIGP-----NKCKCHP 96
      || ||: : : : : : : : : : : : : : : : : : : : : : : : : : : || ||
Db  107  CCPWS-----OKPOEGC-LSDVDFCASANGCCGEGPCCNTVGGFYCRCP 151

QY  97  GYA-----GKTCIQVLRNCGIAPRCKIHRMNTYGSYKCYCLNGYMLMPDG-SCSSALPCS 151
      || |||| : ||| : ||||: || |||| : ||| : ||| : ||| : ||| : |||
Db  152  GYQLQGGDKTC-QDVDECRALINGGQHRVNTGPSYLCECKPGRFLHTDGRTCLAISST 210

QY  152  MAN--COYGC--DVVKGOIRCCPCSPGLQLAPDGRTCVDVDKCATCRASCPFRFCVNTFG 208
      || |||| : |||| : |||| : |||| : |||| : |||| : |||| : ||||
Db  211  ICGNGCGHOCVOLIVTQHRKOC-RPQYQLQHDGRHRCVRSPCAEGNGCGCMH1--CQELRG 267

QY  209  SYICKCHKGFDLMYGKGYQCCHIDIECSLGOYQCSSEFARCYNVRGSYKCKERYQ--GD 266
      || ||| : ||| : ||||: ||| : ||||: ||| : ||||: ||| : ||||: |||
Db  268  LAHGCGHPGYQL--AADHKTCEDVDKALGLAOCAN--GCLNTQGSFKCVCHAGVELCAD 323

QY  267  GLTCVYIPKVMIEPSSGPIHVTPKNG 291
      || ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db  324  GRQCYRIEMEIVN-----SCEANG 343

RESULT 10
T27283
hypothetical protein Y64G10A.f - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T27283
R:Ainscough, R.
submitted to the EMBL Data Library, September 1999
A:Reference number: Z20336
A:Accession: T27283
A:Status: preliminary; translated from GB/EMBL/DDBB
A:Molecule type: DNA
A:Residues: 1-1620 <MIL>
A:Cross-references: EMBL:AL110498; NID:c1542303; PIDN:CA854471.1; CESP:Y64G10A.f
A:Experimental source: clone Y64G10A
C:Genetics:
A:Gene: CESP:Y64G10A.f
A:Introns: 77/1; 116/1; 198/1; 282/1; 365/1; 425/1; 466/1; 548/1; 559/1; 601/1; 625/1;

Query Match          10.9%   Score 357; DB 2; Length 1620;
Best Local Similarity 31.6%; Pred. No. 2.7e-12;
Matches 100; Conservative 30; Mismatches 96; Indels 90; Gaps 17;

```

RESULT 11

T34513
hypothetical protein ZK783.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 *text_change 29-Oct-1999
C:Accession: T34513
R:Pavello, A.; Vaudin, M.
submitted to the EMBL Data Library, August 1994
A:Description: The sequence of C. elegans cosmid ZK783.
A:Reference number: Z21536
A:Accession: T34513
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-3507 <FAM>
A:Cross-references: EMBL:U13646; PIDN:AAC24418.1; GSPDR:GN00021; CFSP:ZK783.1
A:Experimental source: strain Bristol N2; clone ZK783
C:Genetics:
A:Gene: CSP:ZK783.1
A:Map position: 3
A:Introns: 14/1; 48/2; 84/1; 196/3; 303/1; 381/1; 586/1; 605/1; 1175/3; 1207/1; 1409/
3504/1

Query Match 10.5%; Score 346; DB 2; Length 3507;
Best Local Similarity 33.5%; Pred. No. 2.le-11;
Matches 89; Conservative 33; Mismatches 96; Indels 48; Gaps 17;

QY 40 GRIDC--CWGWAROSQCQPFFVILHRIARICOLKAVCPCKKHGEIGLN---KKKC 94
| : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 1564 GSVECEKMGGYKKSQKVCED---INECVAE-----KAPCS---LNANCVNMGTSCSC 1612
| : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
QY 95 HPGYAGK--TCIQVLNECGLIKRPCC--KHRCMNTFGSYKCYCINGYMLMPDG--SCSSAL 148
| : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 1613 KQYRGDGPWCTDI--NECD-ERHPCHPAFCNLKGSFKCEHSGF--KCDGIKKCTNP.L 1668
| : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
QY 149 TCSMANCOYGCD-----VKKGIR--CQFPSPGLQLAPDGRTCVDDECATGRA 195
| : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 1669 ERSCEDVEKPCGRDVHVSCLSVRIKSLSSVCBC-EPIGF-RF-KFSNSCVDIDECPESRN 1727
| : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
QY 196 SC-PREFOCVNTHPSYICKCHKCFDLMYICGYOCHDIDECSLGYOCSSPANCYNVRGS 254
| : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 1728 NCDDPASAVCNTEGYSRCAEGYE----GEGGVCTDIDECDRMGAGCSDMAHCINRMGS 1783
| : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
QY 255 YKCKKRGYOGDLTCVYIPKVMIEP 280
| : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 1784 CGCKCMAGYTGDGATCI---KIPEEP 1806
| : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |

RESULT 12

C36346
fibulin 1 precursor, splice form C - human
N:Alternate names: fibulin C
N:Contains: fibulin 1 splice form A; fibulin 1 splice form C
C:Species: Homo sapiens (man)
C>Date: 19-Apr-1991 #sequence_revision 19-Apr-1991 *text_change 02-Aug-2002
C:Accession: C36346; A36346; A32826
R:Argaves, W.S.; Tran, H.; Burgess, W.H.; Dickerson, K.
J. Cell Biol. 111, 3155-3164, 1990
A>Title: Fibulin is an extracellular matrix and plasma glycoprotein with repeated dom
A:Reference number: A36346; MUID:91100426; PMID:2269669
A:Accession: C36346
A:Molecule type: mRNA
A:Residues: 1-683 <ARG>
A:Cross-references: GH:X53743; NID:g31418; PIDN:CAA37772.1; PID:g31419
A:Accession: A36346
A:Molecule type: mRNA
A:Residues: 1-566 <ARG>
A:Cross-references: GH:X53741; NID:g31414; PIDN:CAA37770.1; PID:g31415
R:Argaves, W.S.; Dickerson, K.; Burgess, W.H.; Ruoslahti, E.
Cell 58, 623-629, 1989
A>Title: Fibulin, a novel protein that interacts with the fibronectin receptor beta-s
A:Reference number: A32826; MUID:89354537; PMID:2527614

DB 333 TCCKNPVNCGRGYHINFEGRTRCVDW--DECAPARPCGKGKRCVNSGSEKCKKTCYVF 490

QY 140 PDG---SCSALTCSM---ANKCYGDDVVKQIQRCQPSGLGLAPAGKTCVIVIDKATG 194

DB 391 -DGISRMCVVNECQYPRGLGKIKCENTIGSYLSCG-SVGFILSVIGSGCELINEF 445

QY 194 RASCPFRFCVNTFGSYICKCHKGFIDIMYIGKYQCHDIDETSL---GQYQSSFAKCYW 251

DB 446 -SSSPGSCANVYGQYCYRRGYQLSDVKG-VTGEDIDCALPTGCHICS YRGINI 501

QY 252 RGSYKCKC-KEGYQ--GIGLTC 270

DB 502 PGSPQCSPPSSGYRIAPNGHC 523

RESULT 14

S78040

N: fibulin, splice form C precursor - mouse

N: Alternate names: basement-membrane protein BM-90

C: Species: Mus musculus (house mouse)

C: Date: 24-Jul-1998 #sequence-revision 24-Jul-1998 #next_change 02 Aug 2002

C: Accession: S78040 #S78560: S36440

R: Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.

R: J. Biochem. 215, 733-740, 1993

A: Title: Sequence of extracellular mouse protein BM-90/fibulin and its calcium depend

A: Reference number: S34968; MIMD:93358897; PMID:854280

A: Accession: S78040

A: Molecule type: mRNA

A: Residues: 1-685 <PAN>

A: Cross-references: EMBL:X70854

R: Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.

submitted to the EMBL data library, January 1993

A: Description: Sequence of extracellular mouse protein BM-90/fibulin and its calcium-

A: Reference number: S36440

A: Accession: S78560

A: Molecule type: mRNA

A: Residues: 1-149, p, 41-685 <CHU>

A: Cross-references: EMBL:X70854

C: Genetics:

C: Introns: 568/3

C: Superfamily: fibulin-1; EGF homology

C: Keywords: alternative splicing; basement membrane; calcium binding; extracellular m

F: 1-29/domain; signal sequence #status predicted <SIG>

F: 30-685/product; fibulin, splice form C #status predicted <MAT>

F: 98,537,541/Binding site; carbohydrate (Asn) (covalent) #status predicted

Query Match 10.28; Score 334.5; DB 2; Length 685;

Best local similarity 28.88; Pred. No. 2,2c-11;

Matches 88; Conservative 32; Mismatches 93; Indels 93; Gaps 15;

QY 56 COPPVLRQRIARICQLKAVCQ----- 78

DB 275 CPDPFICQNTLGSPKRCPLKCKSGFIQDALGNCIDINECLISAPGVGQTINTGSSY 334

QY 79 -----DRCRHC-----RCIGIN-----KCKCHGY 98

DB 335 TCCKNPVNCGRGYILNEGRTRCVWDICAPPACGKGKHCILNSPSPGRCCKAGFYFDG 494

QY 99 AGKTCIOVLNREGGLKP-RPKIKRQMTNTYGYKCYCLNGLYMLMPDG SCSSALTCSMACQ 196

DB 395 ISRTCVDFI-NHCORYPRLGKHKCENTIGSPHSCSAGPRLSVIGKRCFQVNVNFCUNSPCS 454

QY 157 YGCDVWKQIRCCQPSGLGLAP-IDKRTCVIVIDFA--TGKASCPFRFCVNTFGSYICK 214

DB 454 QECANVYGSYOCYC-RRGYQLSDVDGVTEGIDECALPTGCHICS YRGINIIGSFQCS 510

QY 214 C-HKGFIDIMYIGKYQCHDIDETSLGQYQSSFAKCYWVRCSSMC---KCKEGYQCHD 269

DB 511 CPSSGYRIAPNG--RNQDIDECVTGHNCSINETCFNIQCSFRLSFEFENTRRSAFT 568

QY 270 -CVVIP 274

DB 569 KCARIP 574

100
100
100